

RAW SEQUENCE LISTING

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Application Serial Number: 10/598,671

Source: DIPE

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ENTERED

<110> APPLICANT: The UAB Research Foundation
 MARTIN, Michael
 <120> TITLE OF INVENTION: Methods and Compositions Related to
 Regulation of Cytokine Production by Glycogen Synthase
 Kinase 3 (GSK-3)
 <130> FILE REFERENCE: 21085.0072P1

 <140> CURRENT APPLICATION NUMBER:10598671
 <141> CURRENT FILING DATE:0001-01-01
 <150> PRIOR APPLICATION NUMBER: PCT/US05/07586
 <151> PRIOR FILING DATE: 2005-03-17
 <150> PRIOR APPLICATION NUMBER: 60/551,646
 <151> PRIOR FILING DATE: 2004-03-09
 <160> NUMBER OF SEQ ID NOS: 6
 <170> SOFTWARE: FastSEQ for Windows Version 4.0

 <210> SEQ ID NO 1
 <211> LENGTH: 483
 <212> TYPE: PRT
 <213> ORGANISM: Artificial Sequence
 <220> FEATURE:
 <223> OTHER INFORMATION: Description of Artificial Sequence; note =
 synthetic construct
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 Ala Arg Thr Ser Ser Phe Ala Glu Pro Gly Gly Gly Gly Gly Gly Gly
 20 25 30
 Gly Gly Gly Pro Gly Gly Ser Ala Ser Gly Pro Gly Gly Thr Gly Gly
 35 40 45
 Gly Lys Ala Ser Val Gly Ala Met Gly Gly Gly Val Gly Ala Ser Ser
 50 55 60
 Ser Gly Gly Gly Pro Gly Gly Ser Gly Gly Gly Ser Gly Gly Pro
 65 70 75 80
 Gly Ala Gly Thr Ser Phe Pro Pro Pro Gly Val Lys Leu Gly Arg Asp
 85 90 95
 Ser Gly Lys Val Thr Thr Val Val Ala Thr Leu Gly Gln Gly Pro Glu
 100 105 110
 Arg Ser Gln Glu Val Ala Tyr Thr Asp Ile Lys Val Ile Gly Asn Gly
 115 120 125
 Ser Phe Gly Val Val Tyr Gln Ala Arg Leu Ala Glu Thr Arg Glu Leu
 130 135 140
 Val Ala Ile Lys Lys Val Leu Gln Asp Lys Arg Phe Lys Asn Arg Glu
 145 150 155 160
 Leu Gln Ile Met Arg Lys Leu Asp His Cys Asn Ile Val Arg Leu Arg
 165 170 175
 Tyr Phe Phe Tyr Ser Ser Gly Glu Lys Lys Asp Glu Leu Tyr Leu Asn
 180 185 190
 Leu Val Leu Glu Tyr Val Pro Glu Thr Val Tyr Arg Val Ala Arg His
 195 200 205
 Phe Thr Lys Ala Lys Leu Thr Ile Pro Ile Leu Tyr Val Lys Val Tyr
 210 215 220
 Met Tyr Gln Leu Phe Arg Ser Leu Ala Tyr Ile His Ser Gln Gly Val
 225 230 235 240
 Cys His Arg Asp Ile Lys Pro Gln Asn Leu Leu Val Asp Pro Asp Thr
 245 250 255
 Ala Val Leu Lys Leu Cys Asp Phe Gly Ser Ala Lys Gln Leu Val Arg
 260 265 270
 Gly Glu Pro Asn Val Ser Tyr Ile Cys Ser Arg Tyr Tyr Arg Ala Pro
 275 280 285
 Glu Leu Ile Phe Gly Ala Thr Asp Tyr Thr Ser Ser Ile Asp Val Trp

290		295		300											
Ser	Ala	Gly	Cys	Val	Leu	Ala	Glu	Leu	Leu	Leu	Gly	Gln	Pro	Ile	Phe
305					310					315					320
Pro	Gly	Asp	Ser	Gly	Val	Asp	Gln	Leu	Val	Glu	Ile	Ile	Lys	Val	Leu
				325						330					335
Gly	Thr	Pro	Thr	Arg	Glu	Gln	Ile	Arg	Glu	Met	Asn	Pro	Asn	Tyr	Thr
			340					345					350		
Glu	Phe	Lys	Phe	Pro	Gln	Ile	Lys	Ala	His	Pro	Trp	Thr	Lys	Val	Phe
		355					360					365			
Lys	Ser	Arg	Thr	Pro	Pro	Glu	Ala	Ile	Ala	Leu	Cys	Ser	Ser	Leu	Leu
	370					375					380				
Glu	Tyr	Thr	Pro	Ser	Ser	Arg	Leu	Ser	Pro	Leu	Glu	Ala	Cys	Ala	His
385					390					395					400
Ser	Phe	Phe	Asp	Glu	Leu	Arg	Cys	Leu	Gly	Thr	Gln	Leu	Pro	Asn	Asn
			405						410					415	
Arg	Pro	Leu	Pro	Pro	Leu	Phe	Asn	Phe	Ser	Ala	Gly	Glu	Leu	Ser	Ile
			420					425					430		
Gln	Pro	Ser	Leu	Asn	Ala	Ile	Leu	Ile	Pro	Pro	His	Leu	Arg	Ser	Pro
		435					440					445			
Ala	Gly	Thr	Thr	Thr	Leu	Thr	Pro	Ser	Ser	Gln	Ala	Leu	Thr	Glu	Thr
	450					455					460				
Pro	Thr	Ser	Ser	Asp	Trp	Gln	Ser	Thr	Asp	Ala	Thr	Pro	Thr	Leu	Thr
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Asn	Ser	Ser													

<210> SEQ ID NO 2

<211> LENGTH: 420

<212> TYPE: PRT

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence; note = synthetic construct

<400> SEQUENCE: 2

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Val	Gln	Gln	Pro	Ser	Ala	Phe	Gly	Ser	Met	Lys	Val	Ser	Arg	Asp	Lys
			20					25					30		
Asp	Gly	Ser	Lys	Val	Thr	Thr	Val	Val	Ala	Thr	Pro	Gly	Gln	Gly	Pro
		35					40					45			
Asp	Arg	Pro	Gln	Glu	Val	Ser	Tyr	Thr	Asp	Thr	Lys	Val	Ile	Gly	Asn
	50					55					60				
Gly	Ser	Phe	Gly	Val	Val	Tyr	Gln	Ala	Lys	Leu	Cys	Asp	Ser	Gly	Glu
65				70					75					80	
Leu	Val	Ala	Ile	Lys	Lys	Val	Leu	Gln	Asp	Lys	Arg	Phe	Lys	Asn	Arg
			85					90					95		
Glu	Leu	Gln	Ile	Met	Arg	Lys	Leu	Asp	His	Cys	Asn	Ile	Val	Arg	Leu
			100					105					110		
Arg	Tyr	Phe	Phe	Tyr	Ser	Ser	Gly	Glu	Lys	Lys	Asp	Glu	Val	Tyr	Leu
		115					120					125			
Asn	Leu	Val	Leu	Asp	Tyr	Val	Pro	Glu	Thr	Val	Tyr	Arg	Val	Ala	Arg
	130					135					140				
His	Tyr	Ser	Arg	Ala	Lys	Gln	Thr	Leu	Pro	Val	Ile	Tyr	Val	Lys	Leu
145				150						155				160	
Tyr	Met	Tyr	Gln	Leu	Phe	Arg	Ser	Leu	Ala	Tyr	Ile	His	Ser	Phe	Gly
			165					170						175	
Ile	Cys	His	Arg	Asp	Ile	Lys	Pro	Gln	Asn	Leu	Leu	Leu	Asp	Pro	Asp
			180					185					190		
Thr	Ala	Val	Leu	Lys	Leu	Cys	Asp	Phe	Gly	Ser	Ala	Lys	Gln	Leu	Val
	195						200					205			
Arg	Gly	Glu	Pro	Asn	Val	Ser	Tyr	Ile	Cys	Ser	Arg	Tyr	Tyr	Arg	Ala
210					215						220				

Pro	Glu	Leu	Ile	Phe	Gly	Ala	Thr	Asp	Tyr	Thr	Ser	Ser	Ile	Asp	Val
225					230					235					240
Trp	Ser	Ala	Gly	Cys	Val	Leu	Ala	Glu	Leu	Leu	Leu	Gly	Gln	Pro	Ile
				245					250					255	
Phe	Pro	Gly	Asp	Ser	Gly	Val	Asp	Gln	Leu	Val	Glu	Ile	Ile	Lys	Val
			260					265					270		
Leu	Gly	Thr	Pro	Thr	Arg	Glu	Gln	Ile	Arg	Glu	Met	Asn	Pro	Asn	Tyr
		275					280					285			
Thr	Glu	Phe	Lys	Phe	Pro	Gln	Ile	Lys	Ala	His	Pro	Trp	Thr	Lys	Val
	290					295					300				
Phe	Arg	Pro	Arg	Thr	Pro	Pro	Glu	Ala	Ile	Ala	Leu	Cys	Ser	Arg	Leu
305					310					315					320
Leu	Glu	Tyr	Thr	Pro	Thr	Ala	Arg	Leu	Thr	Pro	Leu	Glu	Ala	Cys	Ala
				325					330					335	
His	Ser	Phe	Phe	Asp	Glu	Leu	Arg	Asp	Pro	Asn	Val	Lys	Leu	Pro	Asn
			340					345					350		
Gly	Arg	Asp	Thr	Pro	Ala	Leu	Phe	Asn	Phe	Thr	Thr	Gln	Glu	Leu	Ser
		355					360					365			
Ser	Asn	Pro	Pro	Leu	Ala	Thr	Ile	Leu	Ile	Pro	Pro	His	Ala	Arg	Ile
	370					375					380				
Gln	Ala	Ala	Ala	Ser	Pro	Pro	Ala	Asn	Ala	Thr	Ala	Ala	Ser	Asp	Thr
385					390					395					400
Asn	Ala	Gly	Asp	Arg	Gly	Gln	Thr	Asn	Asn	Ala	Ala	Ser	Ala	Ser	Ala
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Ser	Asn	Ser	Thr												
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<210> SEQ ID NO 3
<211> LENGTH: 2189
<212> TYPE: DNA
<213> ORGANISM: Artificial Sequence
<220> FEATURE:
<223> OTHER INFORMATION: Description of Artificial Sequence; note =
synthetic construct
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gcagcccggg cagcccgagc cccgcagcct gggcctgtgc tcggcgccat gagcggcggc
120
gggccttcgg gaggcggccc tgggggctcg ggcagggcgc ggactagctc gttcgcggag
180
cccggcggcg gaggcggagg aggcggcggc ggccccggag gctcggcctc cggcccaggc
240
ggcaccggcg gcggaagagg atctgtcggg gccatgggtg ggggcgtcgg ggcctcgagc
300
tccggggggtg gacccggcgg cagcggcgga ggaggcagcg gaggccccgg cgcaggcact
360
agcttccccg cgcccggggt gaagctgggc cgtgacagcg ggaaggtgac cacagtcgta
420
gccactctag gccaaggccc agagcgctcc caagaagtgg cttacacgga catcaaagtg
480
attggcaatg gctcatttgg ggtcgtgtac caggcacggc tggcagagac cagggaacta
540
gtcgccatca agaaggttct ccaggacaag aggttcaaga accgagagct gcagatcatg
600
cgtaagctgg accactgcaa tattgtgagg ctgagatact ttttctactc cagtggcgag
660
aagaaagacg agctttacct aaatctggtg ctggaatatg tgcccagagac agtgtaccgg
720
gtggccccgc acttcaccaa ggccaagttg accatcccta tcctctatgt caaggtgtac
780

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840 atgtaccagc tcttccgcag cttggcctac atccactccc agggcgtgtg tcaccgcgac
 900 atcaagcccc agaacctgct ggtggaccct gacactgctg tcctcaagct ctgcgatttt
 960 ggcagtgcaa agcagttggt ccgaggggag cccaatgtct cctacatctg ttctcgctac
 1020 taccggggccc cagagctcat ctttggagcc actgattaca cctcatccat cgatgttttg
 1080 tcagctggct gtgtactggc agagctcctc ttggggccagc ccatcttccc tggggacagt
 1140 ggggtggacc agctggtgga gatcatcaag gtgctgggaa caccaacccg ggaacaaatc
 1200 cgagagatga accccaacta cacggagttc aagttccctc agattaaagc tcacccctgg
 1260 acaaaggtgt tcaaactctg aacgccgcca gaggccatcg cgctctgctc tagcctgctg
 1320 gagtacaccc catcctcaag gctctcccca ctagaggcct gtgcgcacag cttctttgat
 1380 gaactgcat gtctgggaac ccagctgcct aacaaccgcc cacttcccc tctcttcaac
 1440 ttcagtgtg gtgaactctc catccaaccg tctctcaacg ccattctcat cctcctcac
 1500 ttgaggtccc cagcgggcac taccaccctc acccgtcct cacaagcttt aactgagact
 1560 ccgaccagct cagactggca gtcgaccgat gccacaccta ccctcactaa ctctcctga
 1620 gggccccacc aagcaccctt ccacttccat ctgggagccc caagaggggc tgggaagggg
 1680 ggccatagcc catcaagctc ctgccctggc tggggcccta gactagaggg cagaggtaaa
 1740 tgagtccttg tccccacctc cagtccctcc ctcaccagcc tcacccctgt ggtgggcttt
 1800 ttaagaggat tttaactggt tgtggggagg gaagagaagg acaggggtgtt ggggggatga
 1860 ggacctccta ccccttggc cccctccct ccccgagacc tccacctct ccagaccccc
 1920 tccctcctg tgtcccttgt aaatagaacc agcccagccc gtctcctctt ccttccctg
 1980 gccccgggt gtaaatagat tggtataatt ttttcttaa agaaaacgtc gattcgacc
 2040 gtccaacctg gccccgccc tctacagct gtaactccc tctgtctc tgcccccaag
 2100 gtctactccc tctcacccc accctggagg gccaggggag tggagagagc tctgatgtc
 2160 ttagtttcca cagtaagggt tgctgtgta cagacctcg ttcaataaat tattggcatg
 2189 aaaacctgaa aaaaaaaaaa aaaaaaaaaa

<210> SEQ ID NO 4

<211> LENGTH: 1639

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence; note =
synthetic construct

<400> SEQUENCE: 4

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 120 ttgtttttta tagtatataa aaggagttaa aagccaagag gacgaagtct ttttcttttt

180 cttctgtggg agaacttaat gctgcattta tcgttaacct aacaccccaa cataaagaca
 240 aaaggaagaa aaggaggaag gaaggaaaag gtgattcgcg aagagagtga tcatgtcagg
 300 gcggcccaga accacctcct ttgcggagag ctgcaagccg gtgcagcagc cttcagcttt
 360 tggcagcatg aaagttagca gagacaagga cggcagcaag gtgacaacag tgggtggcaac
 420 tcctgggcag ggtccagaca ggccacaaga agtcagctat acagacacta aagtgattgg
 480 aaatggatca tttgggtgtg tatatcaagc caaactttgt gattcaggag aactggtcgc
 540 catcaagaaa gtattgcagg acaagagatt taagaatcga gagctccaga tcatgagaaa
 600 gctagatcac tgtaacatag tccgattgcg ttatttcttc tactccagtg gtgagaagaa
 660 agatgaggtc tatcttaatc tgggtgctgga ctatgttccg gaaacagtat acagagttgc
 720 cagacactat agtcgagcca aacagacgct ccctgtgatt tatgtcaagt tgtatatgta
 780 tcagctgttc cgaagtttag cctatatcca ttcctttgga atctgccatc gggatattaa
 840 accgcagaac ctcttgttgg atcctgatac tgctgtatta aaactctgtg actttggaag
 900 tgcaaagcag ctggtccgag gagaacccaa tgtttcgtat atctgttctc ggtactatag
 960 ggcaccagag ttgatctttg gagccactga ttatacctct agtatagatg tatggctctgc
 1020 tggctgtgtg ttggctgagc tgttactagg acaaccaata tttccagggg atagtgggtgt
 1080 ggatcagttg gtagaaataa tcaaggctct gggaactcca acaagggagc aaatcagaga
 1140 aatgaacca aactacacag aatttaaatt ccctcaaatt aaggcacatc cttggactaa
 1200 ggattcgtca ggaacaggac atttcacctc aggagtgcgg gtcttccgac cccgaactcc
 1260 accggaggca attgcactgt gtagccgtct gctggagtat acaccaactg cccgactaac
 1320 accactggaa gcttgtgcac attcattttt tgatgaatta cgggacccaa atgtcaaact
 1380 accaaatggg cgagacacac ctgcactctt caacttcacc actcaagaac tgtcaagtaa
 1440 tccacctctg gctaccatcc ttattcctcc tcatgctcgg attcaagcag ctgcttcaac
 1500 cccacaaaat gccacagcag cgtcagatgc taatactgga gaccgtggac agaccaataa
 1560 tgctgcttct gcatcagctt ccaactccac ctgaacagtc ccgagcagcc agctgcacag
 1620 gaaaaaccac cagttacttg agtgtcactc agcaacactg gtcacgtttg gaaagaatat
 1639 taaaaaaaaa aaaaaaaaaa

<210> SEQ ID NO 5

<211> LENGTH: 20

<212> TYPE: DNA

<213> ORGANISM: Artificial Sequence

<220> FEATURE:

<223> OTHER INFORMATION: Description of Artificial Sequence; note =
synthetic construct

<400> SEQUENCE: 5